09835992

L30 ANSWER 1 OF 11 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:426134 BIOSIS
DOCUMENT NUMBER: PREV200200426134
TITLE: Serological identification and expression analysis of ***gastric*** cancer-associated genes.
AUTHOR(S): Line, A. (1); Stengrevics, A.; Slucka, Z.; Li, G.; Jankevics, E.; Rees, R. C.
CORPORATE SOURCE: (1) Biomedical Research and Study Centre, University of Latvia, 1 Ratsupites St, LV-1067, Riga: aija@biomed.lu.lv Latvia
SOURCE: British Journal of Cancer, (5 June, 2002) Vol. 86, No. 11, pp. 1824-1830. http://www.nature.com/bjc/. print. ISSN: 0007-0920.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Serological identification of tumour antigens by recombinant expression cloning has proved to be an effective strategy for the identification of cancer-associated genes having a relevance to cancer aetiology and progression, and for defining possible targets for immunotherapeutic intervention. In the present study we applied this technique to identify immunogenic proteins for ***gastric*** cancer that resulted in isolation of 14 distinct serum-reactive antigens. In order to evaluate their role in tumourigenesis and assess the immunogenicity of the identified antigens, we characterised each cDNA clone by DNA sequence analysis, mRNA tissue distribution, comparison of mRNA levels in cancerous and adjacent non-cancerous tissues and the frequency of antibody responses in allogeneic patient and control sera. Previously unknown splice variants of TACC1 and an uncharacterised gene Ga50 were identified. The expression of a newly identified TACC1 isoform is restricted to brain and ***gastric*** cancer tissues. Comparison of mRNA levels by semi-quantitative RT-PCR revealed a relative overexpression of three genes in cancer tissues, including growth factor granulin and Tbdn-1 - an orthologue of the mouse acetyltransferase gene which is associated with blood vessel development. An unusual DNA polymorphism - a three-nucleotide deletion was found in NUCB2 cDNA but its mRNA level was consistently decreased in ***gastric*** tumours compared with that in the adjacent non-cancerous tissues. This study has revealed several new ***gastric*** cancer candidate genes; additional studies are required to gain a deeper insight into their role in the tumorigenesis and their potential as therapeutic targets.

L30 ANSWER 2 OF 11 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2003005972 EMBASE
TITLE: Design of proteome-based studies in combination with serology for the identification of biomarkers and novel targets.
AUTHOR: Seliger B.; Kellner R.
CORPORATE SOURCE: Dr. B. Seliger, Johannes Gutenberg University, IIIrd Dept. of Int. Med., Langenbeckstr. 1, D-55101 Mainz, Germany. b.seliger@3-med.klinik.uni-mainz.de
SOURCE: Proteomics, (1 Dec 2002) 2/12 (1641-1651). Refs: 63 ISSN: 1615-9853 CODEN: PROTC7
COUNTRY: Germany
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 004 Microbiology
016 Cancer
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Recently proteome analysis has rapidly developed in the post-genome era and is now widely accepted as a complementary technology to genetic profiling. The improvement in the technology of both two-dimensional electrophoresis (2-DE) analysis as well as protein identification has made proteomics a valuable and powerful tool to study human diseases. A combination of conventional proteome analysis with serology has been

developed as a promising experimental approach for the discovery of serological markers in different malignancies. However, the design of proteome-based studies has to be carefully performed since there are a number of critical needs for systematic and reproducible proteome analysis. In particular, the selection of tissue and its preparation represent an important step in proteome analysis. Besides the preparation of protein samples, the 2-DE and protein identification is a further critical issue. So far proteome-based technologies have been successfully used in tumor immunnology for the identification of tumor-specific autoantigens. Similarly, this technology has been employed for the detection of virulence factors, antigens and vaccine candidates in infectious diseases, as well as for the identification of diagnostic and prognostic markers, suggesting that proteome-based analysis is a promising tool for the identification of prognostic, diagnostic markers as well as for novel therapeutic targets which could be used for treatment of diseases. The integration of proteome-based approaches with data from genomic or genetic profiling will lead to a better understanding of different diseases, which will then contribute to the direct translation of the research findings into clinical practice.

L30 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:269964 CAPLUS
DOCUMENT NUMBER: 137:336402
TITLE: Preparation of ***SEREX*** -defined tumor antigens and preliminary study of their seroreactivity
AUTHOR(S): Zhang, Huizhen; Wang, Ying; Yuan, Ming; Wang, Shujun; Ji, Ping; Zhou, Guangyan; Ge, Hailiang
CORPORATE SOURCE: Shanghai Institute of Immunology, Shanghai Second Medical University, Shanghai, 200025, Peop. Rep. China
SOURCE: Zhongguo Mianyixue Zazhi (2002), 18(2), 98-101
CODEN: ZMZAEE; ISSN: 1000-484X
PUBLISHER: Zhongguo Mianyixue Zazhi Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB Using ***SEREX*** method, the authors had previously screened a no. of pos. clones from human ovarian cancer cDNA expression libraries. Among them, three full-length genes MY-OVA-2,7 and 13 were cloned and their fusion proteins were expressed in E. Coli. The proteins were purified with affinity chromatog. and thrombin digestion, and characterized by SDS-PAGE and Western Blot. These purified proteins were then applied to test the seroreactivity of 74 patients with different kinds of tumors and 13 healthy controls. The results showed that reactivities against MY-OVA-2 and MY-OVA-7 were detectable in both tumor and normal samples, while reactivity against MY-OVA-13 was only detected in some tumor patients but not in normal subjects. Thus, the recombinant tumor antigens may provide a useful tool for the serodiagnosis of tumors.

L30 ANSWER 4 OF 11 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2003039343 IN-PROCESS
DOCUMENT NUMBER: 22434893 PubMed ID: 12547166
TITLE: Altered splicing pattern of TACC1 mRNA in ***gastric*** cancer.
AUTHOR: Line Aija; Slucka Zane; Stengrevics Aivars; Li Geng; Rees Robert C
CORPORATE SOURCE: Biomedical Research and Study Center, University of Latvia, Riga, Latvia.
SOURCE: CANCER GENETICS AND CYTOGENETICS, (2002 Nov) 139 (1) 78-83.
Journal code: 7909240. ISSN: 0165-4608.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20030128
Last Updated on STN: 20030128
AB Transforming acidic coiled-coil (TACC) proteins are centrosome and microtubule-associated proteins that are essential for mitotic spindle function. We identified TACC1 as an immunogenic protein and a potential

tumor antigen by applying serological identification of antigens by recombinant expression cloning ( ***SEREX*** ) technique to screen a ***gastric*** cancer cDNA library. The 5'RLM-RACE and reverse transcriptase polymerase chain reaction analyses revealed at least six different transcript variants of TACC1 with variable transcription start sites and alternative exon usage (designated TACC1-A-TACC1-F). All transcripts differ in their 5' ends but share an identical 3' region encoding coiled-coil domain. Four transcripts were universally expressed in all normal tissues analyzed but TACC1-D and TACC1-F showed a restricted expression pattern. TACC1-F, a transcript representing the ***SEREX*** -identified cDNA clone, was predominantly expressed in brain and ***gastric*** tumors to a similar level. TACC1-D was only weakly detectable in kidney and colon but not in other normal tissues, while a relatively strong expression was observed in 50% of ***gastric*** cancer tissue samples analyzed. These transcript variants are generated possibly as a result of alterations in efficiency and pattern of alternative splicing; these isoforms may represent genetic markers, for example TACC1-D for ***gastric*** cancer. We also propose that inappropriate expression of the isoforms in ***gastric*** cancer cells might result in dysfunction of TACC1 thus contributing to the genetic instability.

L30 ANSWER 5 OF 11 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001227277 MEDLINE
DOCUMENT NUMBER: 21134339 PubMed ID: 11237751
TITLE: Gene cloning of immunogenic antigens overexpressed in pancreatic cancer.
AUTHOR: Nakatsura T; Senju S; Yamada K; Jotsuka T; Ogawa M; Nishimura Y
CORPORATE SOURCE: Division of Immunogenetics, Department of Neuroscience and Immunology, Kumamoto University Graduate School of Medical Sciences, 2-2-1 Honjo, Kumamoto, 860-0811, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Mar 9) 281 (4) 936-44.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426
AB The serological analysis of recombinant cDNA expression libraries ( ***SEREX*** ) by utilizing a library derived from a human pancreatic adenocarcinoma cell line and IgG antibodies from an allogeneic patient serum led to the identification of 18 genes: 13 of these were known genes, and 5 were unknown genes. In Northern and RT-PCR analyses, we found that the expression of mRNA of 14 genes was elevated in pancreatic cancer cell lines compared with the levels in normal pancreatic tissues. In addition, the expression of mRNA of hsp105 in colon cancer was greater than that in normal colon tissue. Immunohistochemical analysis using anti-hsp105 antibody revealed that an increased expression of hsp105 is a characteristic feature of pancreatic ductal and colon adenocarcinoma. Furthermore, hsp105 immunoreactivity in some cases of ***gastric*** , esophageal, and hepatocellular carcinoma was much stronger than that in normal corresponding tissues. These molecules identified may provide good diagnostic markers for cancer cells.


L30 ANSWER 6 OF 11 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001489843 MEDLINE
DOCUMENT NUMBER: 21423019 PubMed ID: 11531257
TITLE: Expression of multiple cancer-testis antigen genes in gastrointestinal and breast carcinomas.
AUTHOR: Mashino K; Sadanaga N; Tanaka F; Yamaguchi H; Nagashima H; Inoue H; Sugimachi K; Mori M

CORPORATE SOURCE: Department of Surgery, Medical Institute of Bioregulation, Kyushu University, 4546 Tsurumibaru, Beppu, Japan.
SOURCE: BRITISH JOURNAL OF CANCER, (2001 Sep 1) 85 (5) 713-20. Journal code: 0370635. ISSN: 0007-0920.
PUB. COUNTRY: Scotland: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010905
Last Updated on STN: 20021001
Entered Medline: 20011004

AB Cancer-testis antigens (CTAs) such as MAGE are selectively expressed in various types of human neoplasms but not in normal tissues other than testis. This characteristic feature of CTAs makes them promising antigens for cancer-specific immunotherapy. A critical requirement for this therapy is identification of promising antigens. In this study, we investigated the expression of 6 genes recently identified by serological analysis of antigens by recombinant expression ( ***SEREX*** ) libraries: NY-ESO-1, LAGE-1, SCP-1, SSX-1, SSX-2, and SSX-4, in many.surgical samples of gastrointestinal and breast carcinomas using reverse transcription-polymerase chain reaction. We found relatively high expression of SCP-1 (23.5%) and SSX-4 (20.6%) in ***gastric*** carcinoma, LAGE-1 (39.1%) and NY-ESO-1 (23.9%) in oesophageal carcinoma, and SCP-1 (34.1%) in breast carcinoma. We also found frequent synchronous expression with MAGE, including LAGE-1 (46.2%) in oesophageal carcinoma, SSX-4 (46.7%) in ***gastric*** carcinoma, and SCP-1 (38.3%) in breast carcinoma. Immunohistochemical analysis of the tumour samples expressing both MAGE-4 and NY-ESO-1 genes demonstrated differences in distribution between MAGE-4 and NY-ESO-1 in serial sections. We concluded that NY-ESO-1, LAGE-1, SCP-1 and SSX-4 genes may be promising candidates for cancer-specific immunotherapy in addition to MAGE, and that polyvalent cancer vaccines may be useful in cases of heterogeneous expressions of CTA genes in gastrointestinal and breast carcinomas.


L30 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:668660 CAPLUS
DOCUMENT NUMBER: 136:384551
TITLE: Specificity of two new hepatocellular carcinoma antigens
AUTHOR(S): Liao, Hong; Chen, Jianhua; Mo, Farong; Yuan, Zhigang; Chen, Weiping; Kuang, Xiaocong; Luo, Guorong
CORPORATE SOURCE: Department of Histology and Embryology, Guangxi Medical University, Nanning, 530021, Peop. Rep. China
SOURCE: Guangxi Yike Daxue Xuebao (2001), 18(2), 200-201 CODEN: GYDXFJ; ISSN: 1005-930X
PUBLISHER: Guangxi Yike Daxue Xuebao Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB The specificity of two new hepatocellular carcinoma (HCC) antigens (NO.HCC-1-8a and HCC-3-13) to HCC was studied. The specificity of two HCC antigens was identified by recombinant expression cloning technique ( ***SEREX*** ) in allogenic HCC sera and other sera of ***gastric*** carcinoma, breast cancer, and Normal individuals. The cases of antibody-pos. responses to two HCC antigens were 8 and 9 in 10 HCC, 0 and 1 in 5 ***Gastric*** carcinoma, 2 and 2 in 28 normal individuals, and both zero in 10 breast cancer, resp. The results showed that two new HCC antigens had high specificity in HCC cases and may be used as one of serol. diagnostic markers in HCC.

L30 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:885252 CAPLUS
DOCUMENT NUMBER: 135:75413
TITLE: Serological analysis of BALB/c methylcholanthrene sarcoma Meth A by ***SEREX*** : identification of a cancer/testis antigen

AUTHOR(S): Ono, Toshiro; Sato, Shuichiro; Kimura, Nobuhiko; Tanaka, Motoyuki; Shibuya, Akira; Old, Lloyd J.; Nakayama, Eiichi
CORPORATE SOURCE: Department of Immunology, Okayama University Medical School, Okayama, 700-8558, Japan
SOURCE: International Journal of Cancer (2000), 88(6), 845-851
CODEN: IJCNAW; ISSN: 0020-7136
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Antigens of BALB/c methylcholanthrene-induced fibrosarcoma Meth A recognized by the host humoral immune response were investigated by serol. anal. of antigens by recombinant expression cloning ( ***SEREX*** ). Immunoscreening a cDNA library from Meth A (K.gamma.) cells (Meth A retrovirally transfected with murine IFN-.gamma. cDNA) with sera from BALB/c mice growing parental Meth A transplants identified 10 antigens. One of them, OY-MS-4, showed characteristics of a cancer/testis (CT) antigen. Nucleotide sequence anal. revealed that OY-MS-4 was identical to a mouse placenta and embryonic expression gene (pem) known to be selectively expressed during embryogenesis and in transformed cell lines. In adult mice, expression of OY-MS-4 was restricted to testis and placenta. Four of 6 methylcholanthrene-induced fibrosarcomas in BALB/c mice showed strong expression of OY-MS-4. In 6 T-cell leukemias, only a dimethylbenzanthracene-induced leukemia, EL4 (C57BL), showed strong expression. Two other tumors, A20.2J and P815, induced by ethylnitrosourea and methylcholanthrene, resp., also strongly expressed OY-MS-4. The other 9 gene products identified in Meth A by ***SEREX*** were expressed in all 15 tumors tested and in a range of normal tissues. Sequence anal. of cDNA inserts coding for the ***SEREX*** -defined antigens showed no evidence of mutation. Despite the expression of OY-MS-I-10 antigens in methylcholanthrene sarcomas other than Meth A, no antibody was detected in the sera of mice bearing these other sarcomas. The basis for the unique immunogenicity of OY-MS-1-10 presented by Meth A, but not by other syngeneic tumors expressing these gene products, is unknown.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 9 OF 11 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2000419050 MEDLINE
DOCUMENT NUMBER: 20405079 PubMed ID: 10950146
TITLE: ***SEREX*** analysis of ***gastric*** cancer antigens.
AUTHOR: Obata Y; Takahashi T; Sakamoto J; Tamaki H; Tominaga S; Hamajima N; Chen Y T; Old L J
CORPORATE SOURCE: Aichi Cancer Center, Research Institute and Department of Genetics and Pathology, Aichi Cancer Center Hospital, Nagoya, Japan.. yobata@aichi-cc.pref.aichi.jp
SOURCE: CANCER CHEMOTHERAPY AND PHARMACOLOGY, (2000) 46 Suppl S37-42.
Journal code: 7806519. ISSN: 0344-5704.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20000915
Last Updated on STN: 20000915
Entered Medline: 20000906

AB ***Stomach*** cancer is the major malignancy in Japan and one of the most common cancers worldwide. To establish the basis for an immunotherapeutic approach to ***stomach*** cancer, we have initiated an analysis of ***stomach*** cancer antigens recognized by human immunoglobulin G (IgG) antibodies using SE-REX, a powerful expression cloning method developed by Dr. M. Pfreundschuh's group. Five ***stomach*** cancer cDNA libraries have been screened with autologous patient sera: one moderately differentiated adenocarcinoma; two poorly

differentiated adenocarcinomas; and two scirrhous-type poorly differentiated adenocarcinomas of Borrmann type 4, the most devastating form of ***stomach*** cancer. Based on the reactivities of clones with autologous IgG antibodies, an average of 50 independent clones from each library and a total of 297 clones were isolated. DNA sequencing revealed that these 297 clones were derived from 136 different genes. Comparison of the 136 genes to sequences in DNA databases showed that 95 are previously identified genes and 41 are newly identified in this study. The antigens are derived from various genes including a chimeric gene between E-cadherin and an unknown gene Y, AKT oncogene, genes overexpressed in ***stomach*** cancers, genes of which the transcripts are alternatively or aberrantly spliced, and genes known to be involved in autoimmune diseases. Thus ***stomach*** cancer patients can generate an immune response against a surprisingly diverse set of gene products. To identify antigens potentially useful in the diagnosis and therapy of ***gastric*** cancer, all 136 genes were tested for their reactivities with a panel of sera from 44 ***gastric*** cancer patients (17 women and 27 men, aged 35-81 years) and with a panel of sera from 100 control individuals with no previous history of cancer but some of whom had gastritis (55 women and 45 men, aged 30-69 years). Eleven antigens showed reactivity only with a certain proportion of cancer patient sera but not with any control sera. An additional 12 antigens elicited antibody production at a much higher frequency in cancer patients than in control individuals. To evaluate the clinical usefulness of these antigens we are now examining their expression in normal and malignant tissues.

L30 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:81635 CAPLUS
DOCUMENT NUMBER: 130:152119
TITLE: Cancer-associated nucleic acids and antigens from human tissues and their diagnostic and therapeutic applications
INVENTOR(S): Old, Lloyd J.; Scanlan, Matthew J.; Stockert, Elisabeth; Gure, Ali; Chen, Yao-Tseng; Gout, Ivan; O'Hare, Michael; Obata, Yuichi; Pfreundschuh, Michael; Tureci, Ozlem; Sahin, Ugur
PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA; et al.
SOURCE: PCT Int. Appl., 789 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9904265 | A2 | 19990128 | WO 1998-US14679 | 19980715 |
| WO 9904265 | A3 | 19990826 | | |
| W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| US 6218521 | B1 | 20010417 | US 1997-896164 | 19970717 |
| US 6043084 | A | 20000328 | US 1997-948705 | 19971010 |
| US 6403373 | B1 | 20020611 | US 1998-102322 | 19980622 |
| AU 9885715 | A1 | 19990210 | AU 1998-85715 | 19980715 |
| EP 996857 | A2 | 20000503 | EP 1998-936860 | 19980715 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI | | | | |
| JP 2001516009 | T2 | 20010925 | JP 2000-503425 | 19980715 |
| US 2002037541 | A1 | 20020328 | US 2001-835992 | 20010417 |

PRIORITY APPLN. INFO.: US 1997-896164 A 19970717
US 1997-61599P P 19971010

US 1997-61765P P 19971010
US 1997-948705 A 19971010
GB 1997-21697 A 19971011
US 1998-102322 A 19980622
WO 1998-US14679 W 19980715

AB The present invention involves the cloning and sequencing of cDNAs encoding human cancer-assocd. antigen precursors identified by immunoscreening with autologous antisera of subjects having cancer of the breast, colon, ***gastric*** , renal, lung, and prostate tissues. Some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched, whereas other clones are novel but have some homol. to sequences deposited in databases (mainly EST sequences). Several hundred nucleotide and deduced amino acid sequences are provided. Also identified are 86 HLA-binding peptides found in the lung ***SEREX*** clones. The invention also discloses diagnostic and therapeutic methods based upon these mols.

L30 ANSWER 11 OF 11 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999403947 EMBASE
TITLE: ***SEREX*** analysis of ***gastric*** cancer antigens.
AUTHOR: Obata Y.; Takahashi T.
CORPORATE SOURCE: Dr. Y. Obata, Laboratory of Immunology, Aichi Can. Center Research Institute, 1-1 Kanokoden, Chikusa-ku, Nagoya 464-8681, Japan
SOURCE: Biotherapy, (1999) 13/10 (1021-1030).
Refs: 32
ISSN: 0914-2223 CODEN: BITPE
COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
026 Immunology, Serology and Transplantation
027 Biophysics, Bioengineering and Medical Instrumentation
048 Gastroenterology
LANGUAGE: Japanese
SUMMARY LANGUAGE: English; Japanese

AB ***Stomach*** cancer is the major malignancy in Japan and one of most common cancers in the world. To establish the basis for an immunotherapeutic approach to ***stomach*** cancer, we have initiated an analysis of ***stomach*** cancer antigens recognized by human IgG antibodies, using ***SEREX*** , a powerful expression cloning method. Five ***stomach*** cancer cDNA libraries have been screened with autologous patient sera. An average of 50 independent clones were isolated from each library. DNA sequencing revealed that these 297 clones were derived from 136 different genes. Comparison of the 136 genes to sequences in DNA databases showed that 95 are previously identified genes in humans and 41 have been newly identified in this study. The antigens are derived from various genes including a chimeric gene between E-cadherin and an unknown gene Y, the AKT oncogene, genes over-expressed in ***stomach*** cancers, genes whose transcripts are alternatively or aberrantly spliced and genes known to be involved in autoimmune diseases. Thus, ***stomach*** cancer patients can generate an immune response against a surprisingly diverse set of gene products. To select antigens potentially useful in the diagnosis and therapy of ***gastric*** cancer, all 136 were tested for their reactivities with a panel of sera from 44 ***gastric*** cancer patients and with a panel of sera from 100 control individuals with no previous history of cancer but some with gastritis. Eleven antigens showed the reactivity only with a certain proportion of sera from cancer patients, but not with any control sera. An additional dozen antigens elicited antibody production at a much higher frequency in cancer patients than in control individuals. To evaluate the usefulness of these antigens in clinical application, we are now examining their expression in normal and malignant tissues.

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(FILE 'HOME' ENTERED AT 10:49:19 ON 06 FEB 2003)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 10:49:29 ON 06 FEB 2003
L1 1275 S STEROL CARRIER PROTEIN
L2 612035 S GASTRIC OR STOMACH
L3 0 S L1 AND L2
L4 45012 S AUTOANTIBODY
L5 0 S L1 AND L4
L6 314 S SEREX
L7 0 S L6 AND L1
L8 3035375 S CANCER OR TUMOR OR TUMOUR
L9 47 S L1 AND L8
L10 23 DUP REM L9 (24 DUPLICATES REMOVED)
L11 1192841 S ANTIGEN
L12 10 S L11 AND L1
L13 8 DUP REM L12 (2 DUPLICATES REMOVED)
L14 401 S NONSPECIFIC LIPID TRANSFER PROTEIN
L15 0 S L14 AND L2
L16 0 S L14 AND L4
L17 0 S L14 AND L6
L18 16 S L14 AND L8
L19 6 DUP REM L18 (10 DUPLICATES REMOVED)
L20 8 S L14 AND L11
L21 3 DUP REM L20 (5 DUPLICATES REMOVED)
L22 5134 S TUMOR ASSOCIATED ANTIGEN
L23 0 S L22 AND (L1 OR L14)
L24 1548 S AUTOIMMUNO?
L25 212224 S AUTOIMMUN?
L26 0 S L25 AND (L1 OR L14)
L27 814 S CANCER ASSOCIATED ANTIGEN
L28 0 S L27 AND (L1 OR L14)
L29 21 S L6 AND L2
L30 11 DUP REM L29 (10 DUPLICATES REMOVED)
L31 136001 S AUTOLOGOUS
L32 0 S L31 AND (L1 OR L14)

| | Hits | Search Text | DBs | Time Stamp |
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